



OIPE

## RAW SEQUENCE LISTING

DATE: 02/05/2002

PATENT APPLICATION: US/09/916,780A

TIME: 11:44:56

Input Set : A:\REVISED SEQUENCE .0066.txt

Output Set: N:\CRF3\02052002\I916780A.raw

**Does Not Comply**  
**Corrected Diskette Needed**

2 <110> APPLICANT: University of Connecticut  
 3 LI, Yi O'Donnell, Colum Duan, Hui Wu, Yan McAvoy, Richard  
 5 <120> TITLE OF INVENTION: Methods for the Controlled, Automatic Excision of  
 Heterologous DNA from  
 6 Transgenic Plants and DNA-Excising Gene Cassettes for Use Therein  
 8 <130> FILE REFERENCE: 883933.0066  
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/09/916,780A  
 C--> 9 <141> CURRENT FILING DATE: 2001-07-27  
 9 <150> PRIOR APPLICATION NUMBER: US 60/221,318  
 10 <151> PRIOR FILING DATE: 2000-07-28  
 W--> 11 <160> NUMBER OF SEQ ID: 11  
 12 <170> SOFTWARE: PatentIn version 3.0

## ERRORED SEQUENCES

505 <210> SEQ ID NO: 11  
 506 <211> LENGTH: 426  
 507 <212> TYPE: DNA  
 508 <213> ORGANISM: Tobacco vein mottling virus  
 W--> 509 <400> SEQUENCE: 11  
 510 cggaaggatg gtaattatag gtacccatgc tgctgcgtca ctctcgaaga tggtagtcca 60  
 512 atgtactcag agcttaaaat gccaacgaaa aatcatctag taattggcaa ttcaggggat 120  
 514 ccgaaatact tggatctacc aggtgaaatt agcaatctta tgtacatagc aaaggaagga 180  
 516 tattgttata tcaacatatt tcttgcaatg cttgttaatg ttgatgaagc taacgccaaag 240  
 518 gactttacta agagagtgag ggacgagtcg gtacaaaagc ttggaaagtg gccaaagtta 300  
 520 atagatgtcg caactgaatg tgccttacta tctacatatt atcctgcggc ggctagtgcg 360  
 522 gaactaccca ggcttctagt agatcatgot caaaagacaa ttcacgttgt ggattcttat 420  
 524 gggtcgcg 426  
 E--> 528 C&IdOc:.stmLib1:918590.1 11/16/01 *delete*

## VERIFICATION SUMMARY

DATE: 02/05/2002

PATENT APPLICATION: US/09/916,780A

TIME: 11:44:58

Input Set : A:\REVISED SEQUENCE .0066.txt

Output Set: N:\CRF3\02052002\I916780A.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:11 M:283 W: Missing Blank Line separator, <160> field identifier  
L:18 M:283 W: Missing Blank Line separator, <400> field identifier  
L:26 M:283 W: Missing Blank Line separator, <400> field identifier  
L:84 M:283 W: Missing Blank Line separator, <400> field identifier  
L:95 M:283 W: Missing Blank Line separator, <400> field identifier  
L:145 M:283 W: Missing Blank Line separator, <400> field identifier  
L:181 M:283 W: Missing Blank Line separator, <400> field identifier  
L:223 M:283 W: Missing Blank Line separator, <400> field identifier  
L:413 M:283 W: Missing Blank Line separator, <400> field identifier  
L:443 M:283 W: Missing Blank Line separator, <400> field identifier  
L:453 M:283 W: Missing Blank Line separator, <400> field identifier  
L:509 M:283 W: Missing Blank Line separator, <400> field identifier  
L:528 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:445 SEQ:11  
L:528 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:24  
L:528 M:112 C: (48) String data converted to lower case,  
L:528 M:252 E: No. of Seq. differs, <211>LENGTH:Input:426 Found:445 SEQ:11